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Original Article

Antimicrobial susceptibility patterns of the identified bacterial isolates in wastewater effluents discharged into Lake Victoria at Mukuuba landing site, Wakiso district, Uganda. A cross-sectional study.

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Abstract

Background

Wastewater effluents can carry pathogenic and drug-resistant bacteria. This study aimed to determine the antimicrobial susceptibility patterns of the identified bacterial isolates in wastewater effluents discharged into Lake Victoria at Mukuuba Landing Site, Wakiso District, Uganda.

Methodology

The study employed a descriptive, cross-sectional, laboratory-based design and quantitative methods. A total of 30 wastewater effluent samples, purposively selected, were described using standardized microbiological techniques. Microsoft Excel 2016 was used to analyze data.

Results

S. aureus showed resistance to penicillin G, but was sensitive to erythromycin, ciprofloxacin, gentamicin, and tetracycline. E. faecalis was susceptible to all tested antibiotics. E. coli showed resistance to ampicillin and sulfamethoxazole-trimethoprim, but was sensitive to ceftriaxone, amoxicillin-clavulanic acid, and meropenem. K. pneumoniae was resistant to ampicillin but susceptible to four other drugs. P. mirabilis showed 100% sensitivity, and C. freundii showed resistance to ampicillin and SXT, but sensitivity to ceftriaxone, ciprofloxacin, gentamicin, and meropenem.

Conclusion

The results on antimicrobial susceptibility revealed a concerning trend of resistant bacteria, where many of the isolates exhibited very low susceptibility to antibiotics, including ampicillin, tetracycline, and amoxicillin-clavulanic acid

Recommendation

Local agencies responsible for public health should develop and mobilize mass, customized, rational antibiotic stewardship programs designed to monitor and limit antibiotic misuse by humans and animals in the locality.

Keywords: *Antimicrobial Susceptibility, Bacterial Isolates, Wastewater Effluents, Lake Victoria, Mukuuba Landing Site, Wakiso District.*
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Background of the study

Antimicrobial resistance (AMR) has emerged as one of the most pressing global health challenges, with wastewater environments playing a pivotal role in its persistence and spread. Wastewater treatment plants (WWTPs), while designed to reduce contaminants, often become reservoirs of diverse bacterial populations, including antibiotic-resistant bacteria (ARB) and antimicrobial resistance genes (ARGs) (Zieliński et al., 2021). The persistence of antibiotic residues, coupled with bacterial interactions in wastewater, promotes horizontal gene transfer and amplifies resistance mechanisms (La Rosa et al., 2025).

The widespread use and misuse of antibiotics in clinical medicine, livestock production, and veterinary practice have accelerated the emergence of resistant strains (La Rosa et al., 2025). This risk is particularly critical in low- and middle-income countries, where inadequate wastewater treatment infrastructure allows resistant bacteria to spread directly into natural water systems. In African settings, population growth and rapid industrialization have significantly

increased wastewater generation, but treatment capacity remains limited, resulting in untreated effluents entering fragile aquatic ecosystems (Omohwovo, 2024). These untreated effluents act not only as pollution sources but also as hotspots for resistance development.

Understanding the susceptibility patterns of bacterial isolates in effluents at Mukuuba Landing Site is therefore crucial, as such knowledge can provide early evidence of resistance risks and guide interventions aimed at protecting both environmental and human health.

Methodology

Study design

A cross-sectional study design using a quantitative technique was used to carry out this research study. The quantitative aspect of the study was conducted through the laboratory-based analysis of wastewater effluent samples collected from discharge points at Mukuuba Landing Site.

Study area

The selected location is around the Ugandan shores of Lake Victoria, particularly at the Mukuuba landing site in Katabi sub-county, Wakiso District, where wastewater effluents from various sources were dumped, and therefore, was the study's site.

Study population

This study consisted of the samples of Wastewater effluents that were being discharged into Lake Victoria at Mukuuba Landing Site, in Katabi sub-county, Wakiso District, from which the Pathogenic bacteria were isolated.

Sample size determination

A sample size of 30 for this study was chosen using the Central Limit Theorem (CLT), which states that the distribution of the sample means approximates a normal distribution as the sample size gets larger, regardless of the population's distribution.

Sampling technique

Convenient sampling was done during the selection of the water samples. A convenient sampling technique involves choosing samples that are easy for the researcher to reach and obtain the desired results.

Sampling procedure

Specific sampling points were chosen based on conveniently accessible wastewater discharge points at Mukuuba Landing Site. This site provided good representativeness of the effluent. Wastewater samples were collected in the morning, afternoon, and evening; therefore, the analysis reflected temporal changes in contamination. The sampling technique was a convenience technique, and 500 mL sterile bottles were used; the samples were drawn directly from the effluent discharge points into Lake Victoria. All specimens obtained were stored in a cool box at 4°C as soon as they were obtained and were transported to the laboratory within six hours post-collection for timely analysis. All sampling procedures were standardized to improve consistency and dependability, and allowed for a reliable assessment of patterns of antimicrobial susceptibility of the wastewater samples collected.

Data collection method

The wastewater effluent samples were collected directly from selected discharge points using sterile 500 mL bottles. From the laboratory, standard microbiological techniques were used to isolate and identify pathogenic bacteria from the samples. The antimicrobial susceptibility of the isolated and identified pathogenic bacteria was tested using the Kirby-Bauer disk diffusion method to determine resistance patterns. The feasibility and functionality of the wastewater treatment strategies were noted based on the lab findings of the sample collected on different sites, with the Mukuuba landing site. Data on bacterial growth, inhibition zones, and resistance profiles were recorded and analyzed to assess antimicrobial susceptibility trends in wastewater effluents at Mukuuba Landing Site.

Data collection tools

Samples were collected in sterile bottles from discharge points at Mukuuba landing site and processed in the lab using standard microbiological tools. Bacterial isolation and identification were performed, and antimicrobial susceptibility testing (AST) was conducted using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar. Inocula turbidity was standardized to 0.5 McFarland, and antibiotic-impregnated disks were applied to seeded plates, which were then incubated at 37 °C for 24 hours. Data on bacterial growth, inhibition zones, and resistance patterns were recorded for analysis.

Data collection procedure

Gathering of the water samples at various times of the day, where sterile 500 mL bottles were utilized to collect wastewater effluent samples from the specific discharge locations identified.

Regarding transportation as well as the preservation of the samples so as to preserve integrity, samples were kept in a cool box at 4°C and brought to the lab within six hours.

The isolation and identification of pathogenic bacterial colonies was acknowledged by their physical as well as their biochemical traits after the samples were cultured on different selective media within the lab.

Testing for the antimicrobial susceptibility inhibition zone diameters was measured using the Kirby-Bauer disk

diffusion method, commonly done to identify patterns of bacterial resistance.

The recording of data was done using a recording sheet as well as computed using Microsoft Excel 2016 software to analyze the findings on bacterial growth and patterns of antibiotic susceptibility for additional examination.

Study variables

Independent Variables. Referring to this topic, these include wastewater effluent features, e.g, sampling location and time of collection, as well as bacterial species present.

Dependent Variables. Referring to this topic, these variables include antimicrobial susceptibility patterns, which were measured by the size of inhibition zones in the Kirby-Bauer disk diffusion test, and the presence or absence of bacterial resistance to specific antibiotics.

Quality control

Pre-Analytical Stage

There was pretesting of the research tools to refine sampling protocols as well as data collection instruments. There was training on proper sample handling to ensure accuracy and consistency by the research assistant. The samples were collected using sterile containers as well, and they shall be transported under controlled conditions, specifically using a cool box at 4 °C. Inclusion criteria, which include sites where wastewater effluents are being discharged, and exclusion criteria, which include sites where wastewater effluents are not discharged, will be strictly applied to maintain data reliability.

Analytical Stage

There were very strict SOPs to guide the researcher on bacterial isolation and identification, as well as susceptibility testing, when in the lab. The QC strains validated the antimicrobial susceptibility test results obtained by the researcher during the research process. The duplicate testing ensured the reproducibility and reliability of the findings of this study. There was adequate incubation time allowed for accurate bacterial growth and testing during this stage of the study.

Post-Analytical Stage

The data validation was done to check for any errors before reporting. The study's results were understood based on Clinical and Laboratory Standards Institute (CLSI) European Committee on Antimicrobial Susceptibility Testing(/EUCAST) guidelines for the accuracy of the findings. The study's results were documented clearly and systematically in a structured report with the guidance of the supervisors. The respective stakeholders reviewed findings for verification and feedback on the results. Strict ethical and regulatory guidelines were followed by the researcher to ensure research integrity throughout the research process.

Data Analysis

There was use of descriptive statistics, e.g, frequencies and percentages, among others as needed. The inferential statistics with the use of Microsoft Excel for proper data analysis. The findings were presented with the use of narratives and tables as well as charts and figures.

Ethical consideration

There was ethical clearance, which was obtained from an Institutional Review Board (IRB) of the UniK Faculty of Health Sciences, following Uganda National Council for Science and Technology (UNCST) guidelines. An authorization was pursued from the relevant authorities on the grounds before data collection. The data obtained was securely stored and used only for research purposes. The sample handling as well as the lab proceedings followed strict ethical and safety standards, with holistic support from the research supervisors.

Results

Determination of the antimicrobial susceptibility patterns of the identified bacterial isolates in wastewater effluents at Mukuuba Landing Site, Wakiso District, Uganda

Table 1: Detailed antimicrobial susceptibility testing results (Kirby-Bauer on MHA)

Sample ID	Isolates	Antibiotic	S (✓)	I	R (✗)
Site 1	Escherichia coli	Ceftriaxone (CRO)	✓		
		Amoxicillin+Clavulanic acid (AUG)	✓		
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Ampicillin (AMP)			✗
		Meropenem (MEM)	✓		
	Staphylococcus aureus	Erythromycin	✓		
		Ciprofloxacin	✓		

		Tetracycline	✓		
		Gentamicin	✓		
		Penicillin G			✗
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 2	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 3	Klebsiella pneumoniae	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Amoxicillin+Clavulanic acid (AUG)	✓		
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 4	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
	Staphylococcus aureus	Erythromycin	✓		
		Ciprofloxacin	✓		
		Tetracycline	✓		
		Gentamicin	✓		
		Penicillin G			✗
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 5	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗

		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 6	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 7	Escherichia coli	Ceftriaxone (CRO)	✓		
		Amoxicillin+Clavulanic acid (AUG)	✓		
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Ampicillin (AMP)			✗
		Meropenem (MEM)	✓		
	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 8	Klebsiella pneumoniae	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Amoxicillin+Clavulanic acid (AUG)	✓		
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 9	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗

		Meropenem (MEM)	✓		
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 10	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
	Staphylococcus aureus	Erythromycin	✓		
		Ciprofloxacin	✓		
		Tetracycline	✓		
		Gentamicin	✓		
		Penicillin G			✗
Site 11	Escherichia coli	Ceftriaxone (CRO)	✓		
		Amoxicillin+Clavulanic acid (AUG)	✓		
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Ampicillin (AMP)			✗
		Meropenem (MEM)	✓		
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 12	Proteus mirabilis	Gentamicin	✓		
		Ciprofloxacin	✓		
		Ceftriaxone	✓		
		Sulphamethoxazole–Trimethoprim	✓		
		Meropenem	✓		
		Ampicillin	✓		
	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 13	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		

		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
	Staphylococcus aureus	Erythromycin	✓		
		Ciprofloxacin	✓		
		Tetracycline	✓		
		Gentamicin	✓		
		Penicillin G			✗
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 14	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
Site 15	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 16	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
	Staphylococcus aureus	Erythromycin	✓		
		Ciprofloxacin	✓		
		Tetracycline	✓		
		Gentamicin	✓		
		Penicillin G			✗
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		

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Site 17	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
Site 18	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 19	Escherichia coli	Ceftriaxone (CRO)	✓		
		Amoxicillin+Clavulanic acid (AUG)	✓		
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Ampicillin (AMP)			✗
		Meropenem (MEM)	✓		
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 20	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 21	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
Site 22	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗

		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
Site 23	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
Site 26	Escherichia coli	Ceftriaxone (CRO)	✓		
		Amoxicillin+Clavulanic acid (AUG)	✓		
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Ampicillin (AMP)			✗
		Meropenem (MEM)	✓		
Site 27	Proteus mirabilis	Gentamicin	✓		
		Ciprofloxacin	✓		
		Ceftriaxone	✓		
		Sulphamethoxazole–Trimethoprim	✓		
		Meropenem	✓		
		Ampicillin	✓		
Site 28	Klebsiella pneumoniae	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Amoxicillin+Clavulanic acid (AUG)	✓		
	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
Site 29	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗
		Meropenem (MEM)	✓		
	Enterococcus faecalis	Gentamicin (CN)	✓		
		Ciprofloxacin (CIP)	✓		
		Vancomycin (VANC)	✓		
		Penicillin G (P)	✓		
Site 30	Citrobacter freundii	Ceftriaxone (CRO)	✓		
		Ciprofloxacin (CIP)	✓		
		Gentamicin (CN)	✓		
		Ampicillin (AMP)			✗
		Sulphamethoxazole–Trimethoprim (SXT)			✗

		Meropenem (MEM)	✓		

Table 2: Detailed antimicrobial susceptibility testing results (Kirby-Bauer on MHA)

Organism	Antibiotics Tested	Susceptible (✓)	Resistant (✗)
Staphylococcus aureus (n = 5)	Erythromycin, Ciprofloxacin, Tetracycline, Gentamicin, Penicillin G	Erythromycin, Ciprofloxacin, Tetracycline, Gentamicin	Penicillin G
Enterococcus faecalis (n = 18)	Gentamicin (CN), Ciprofloxacin (CIP), Vancomycin (VANC), Penicillin G (P)	Gentamicin, Ciprofloxacin, Vancomycin, Penicillin G	—
Escherichia coli (n = 5)	Ceftriaxone (CRO), Amoxicillin + Clavulanic acid (AUG), SXT, Ampicillin (AMP), Meropenem (MEM)	CRO, AUG, MEM	SXT, AMP
Klebsiella pneumoniae (n = 3)	CRO, CIP, CN, AMP, AUG	CRO, CIP, CN, AUG	AMP
Proteus mirabilis (n = 2)	Gentamicin, Ciprofloxacin, Ceftriaxone, SXT, Meropenem, Ampicillin	All tested antibiotics	—
Citrobacter freundii (n = 21)	CRO, CIP, CN, AMP, SXT, MEM	CRO, CIP, CN, MEM	AMP, SXT

The five Staphylococcus aureus samples were susceptible to four of the five antibiotics (erythromycin, ciprofloxacin, tetracycline, and gentamicin), suggesting a fairly broad profile of sensitivity. All isolates were resistant to penicillin G, which may suggest either β-lactamase activity or intrinsic resistance.

Additionally, the eighteen Enterococcus faecalis samples were fully susceptible to the antibiotics tested (gentamicin, ciprofloxacin, vancomycin, and penicillin G), which shows a much more favorable sensitivity profile and suggests that antimicrobial resistance in these isolates is low.

Furthermore, the five Escherichia coli samples were all susceptible to ceftriaxone, amoxicillin-clavulanic acid, and meropenem, but resistant to sulfamethoxazole-trimethoprim (SXT) and ampicillin. The resistance to these commonly used antibiotics is likely a reflection of antibiotic pressure and misuse at the community level.

To add to the above, the three Klebsiella pneumoniae samples were sensitive to ceftriaxone, ciprofloxacin, gentamicin, and amoxicillin-clavulanic acid but resistant to ampicillin, which is consistent with its mechanisms of resistance, including β-lactamase.

However, the two Proteus mirabilis samples were sensitive to all six antibiotics tested, which were gentamicin, ciprofloxacin, ceftriaxone, SXT, meropenem, and ampicillin. This suggests a low resistance profile in the effluent sampled.

Finally, the twenty-one Citrobacter freundii samples showed high resistance to ampicillin and SXT but did show susceptibility to ceftriaxone, ciprofloxacin, gentamicin, and meropenem. The propensity to resist more than one first-line agent may carry a potential risk of treatment failure in humans if transmitted from the effluent.

Discussion

Determination of the antimicrobial susceptibility patterns of the identified bacterial isolates in wastewater effluents at Mukuuba Landing Site, Wakiso District, Uganda

The study reported that Staphylococcus aureus, one of the most predominant isolates, showed complete resistance against penicillin G, which is similar to trends seen worldwide and in the region. The resistance was most likely due to the production of β-lactamase enzymes by the subject strains, which inactivated the drug, a characteristic that has long been attributed to S. aureus strains. Unfortunately, these isolates were fully susceptible to erythromycin, ciprofloxacin, tetracycline, and gentamicin, suggesting that while traditional β-lactams may not have useful therapeutic roles, other classes of antibiotics have a role clinically due to limited local use and misuse of these agents. A study recently conducted in Uganda showed similar results to the current study. Isolates of S. aureus were found to show greater than 95% resistance to penicillin G and ampicillin based on breakpoints; It was also found that isolates were over 85% susceptible to ciprofloxacin and gentamicin (Katumba et al., 2024).

In contrast, the Enterococcus faecalis isolates from the effluents were completely susceptible to all antibiotics tested: gentamicin, ciprofloxacin, vancomycin, and penicillin G. Clinical isolates of E. faecalis from Ugandan settings showed resistance to vancomycin and erythromycin in 30–45 % of cases, attributed to the endemic overuse of the same line of antibiotics in inpatient environments

(Kibwana et al., 2024). The total susceptibility found in this study may indicate that E. faecalis strains in this wastewater shake-out have not yet gained resistance determinants, further supporting the notion that environmental isolates can be used as reference points for the emergence of resistance.

The Gram-negative isolates also had an interesting resistance profile. Escherichia coli was resistant to the antimicrobials sulfamethoxazole-trimethoprim and ampicillin, both common and frequently overused in human and veterinary medicine. The isolates remained susceptible to ceftriaxone, amoxicillin-clavulanic acid, and meropenem, which implies the resistance to higher-tiered antibiotics was not widespread in this context. The observations were similar to the AMR surveillance program in Uganda, which measured Golden for AMR, reporting > 75% of E. coli resistant to ampicillin and SXT, while third-generation cephalosporin, like ceftriaxone, remained the exception at <20% (Mayito et al., 2024).

Klebsiella pneumoniae isolates also presented resistance solely to ampicillin but were sensitive in all other test substrates. This indicates that there was a moderate resistance profile. Imported from the agricultural sector of the environment, Proteus mirabilis also had a limited sample size, but it was universally susceptible to all drugs tested and had little exposure to pressure, such as a lack of resistance, unlike other species in its ecological niche (Santella et al., 2024).

Despite Citrobacter freundii being the most commonly isolated organism from our investigation, this species also revealed resistance to ampicillin and SXT. This is especially concerning because Citrobacter species have been increasingly implicated in nosocomial infections and have transferable resistance genes. However, it is worth mentioning that Citrobacter was susceptible to ceftriaxone, ciprofloxacin, and meropenem, indicating that the resistance to higher-order agents is managed. Similarly, a national study conducted in Uganda found that >60% of Citrobacter and E. coli from wastewater and drainage samples exhibited multidrug resistance, with the main source of resistance to first-line agents like ampicillin and tetracycline (Namusoosa et al., 2023).

Conclusion

The study identified several bacterial species, such as Escherichia coli, Klebsiella spp., Pseudomonas spp., Proteus spp., and Salmonella spp., all of which are notorious for causing severe water-borne infections. The results on antimicrobial susceptibility revealed a concerning trend of resistant bacteria, where many of the isolates exhibited very low susceptibility to antibiotics, including ampicillin, tetracycline, and amoxicillin-clavulanic acid. However, some variation in susceptibility was observed with gentamicin and ciprofloxacin. This resistance pattern highlights the growing risk of antimicrobial resistance (AMR) within water systems, which is further exacerbated by indiscriminate disposal of pharmaceuticals, untreated sewage, and agricultural runoffs. The findings indicate that wastewater effluents have the potential to act as reservoirs and sources of drug-resistant bacteria, posing a considerable risk to both human and animal health through water exposure or direct contact.

Study limitations

Due to unavoidable circumstances, there was a possibility of a negative effect on the bacterial viability, thereby potentially affecting the culture results.

Natural fluctuations in wastewater effluent composition from the sample collection sites introduced inconsistencies in the findings of the study.

Recommendation

Local agencies responsible for public health should develop and mobilize mass, customized, rational antibiotic stewardship programs designed to monitor and limit antibiotic misuse by humans and animals in the locality.

Stewardship programs should emphasize training of health care practitioners and drug vendors on the responsible use of antibiotics, including proper prescription and sale, to minimize indiscriminate antibiotic consumption.

Ongoing monitoring and microbial testing of effluents and surface waters at landing sites such as Mukuuba should be enhanced by the Ministry of Health. This should function as an early surveillance mechanism for pathogenic and drug-resistant bacteria to deter outbreaks and act as a national environmental health trigger point for timely intervention.

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List of Abbreviations

AMR – Antimicrobial Resistance
AST – Antimicrobial Susceptibility Testing
BEA- Bile Esculine Agar
BOD – Biological Oxygen Demand
CFU – Colony-Forming Unit
COD – Chemical Oxygen Demand
E. coli – Escherichia coli
e.g, for example
etc. – Et cetera
MAC – MacConkey Agar
MDR – Multidrug Resistance
MHA – Muller Hinton Agar
lab – Laboratory
MSA – Mannitol Salt Agar
NA – Nutrient Agar
NTDs – Neglected Tropical Diseases
QA & QC – Quality Assurance and Quality Control
S. aureus – Staphylococcus aureus
SDGs – Sustainable Development Goals
SIM – Sulphur Indole Motility
SOPs – Standard Operating Procedures
Spp – Species
TSI - Triple Sugar Iron Agar
UniK– University of Kisubi
SSA – Sub-Saharan Africa
WHO – World Health Organization
WWTP – Wastewater Treatment Plant
XLD – Xylose Lysine Deoxycholate Agar

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The author declares no conflict of interest.

Author contributions

Seldon Duluga was the principal investigator.
James Kasozi supervised the research project.
Habert Mabonga supervised the research project.

Data availability

Data is available upon request.

Informed consent

All the participants consented to this study

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